

IN THE CLAIMS

Please amend the claims as follows:

Claims 1-43 (Cancelled)

Claim 44 (Currently Amended): An isolated coryneform bacterium, which expresses has been modified to express a decreased amount of malate dehydrogenase or to express a malate dehydrogenase with decreased activity the product of the mdhA gene (malate dehydrogenase) compared to the corresponding unmodified starting strain, wherein said malate dehydrogenase has at least 90-95% homology to SEQ ID NO: 3.

Claim 45 (Currently Amended): The isolated coryneform bacterium of Claim 44, wherein the [[mdhA]] gene encoding malate dehydrogenase has been eliminated.

Claim 46 (Currently Amended): The isolated coryneform bacterium of Claim 44, wherein the [[mdhA]] gene encoding malate dehydrogenase has been inactivated.

Claim 47 (Currently Amended): The isolated coryneform bacterium of Claim 44, wherein the [[mdhA]] gene encoding malate dehydrogenase has been attenuated by modification of at least one repressor gene, activator gene, operator, promoter, attenuator, ribosome binding site, or start codon, start codon, or other signal structure which is operably associated with said mdhA gene.

Claim 48 (Currently Amended): The isolated coryneform bacterium of Claim 44, which expresses a malate dehydrogenase with decreased activity compared to the

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corresponding unmodified strain wherein the *mdhA* gene has been attenuated by a modification which reduces the enzyme activity of the *mdhA* gene product.

Claim 49 (Previously Presented): The isolated coryneform bacterium of Claim 44, which is of the genus *Corynebacterium* or *Brevibacterium*.

Claim 50 (Currently Amended): The isolated coryneform bacterium of Claim 44, which is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, [[,]] *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

Claim 51 (Previously Presented): The isolated coryneform bacterium of Claim 44 which comprises pEMmdhAint.

Claim 52 (Currently Amended): A process for making an L-amino acid comprising:  
a) culturing the bacterium of Claim 44 in [[an]] a medium suitable for the production of said L-amino acid by fermentation, and  
b) recovering said L-amino acid from the culture medium or from the bacterial cells.

Claim 53 (Previously Presented): The process of Claim 52, wherein said amino acid is L-lysine.

Claim 54 (Previously Presented): The process of Claim 52, wherein said amino acid is L-glutamate.

Claim 55 (Currently Amended): The process of Claim 52, wherein in said bacterium the *mdhA* gene has been eliminated or inactivated.

Claim 56 (Currently Amended): The process of Claim 52, wherein in said bacterium the [[*mdhA*]] gene encoding malate dehydrogenase has been attenuated by modification of at least one ~~repressor gene, activator gene~~, operator, promoter, attenuator, ribosome binding site, or start codon, start codon, or other signal structure which is operably associated with said *mdhA* gene.

Claim 57 (Currently Amended): The process of Claim 52, wherein [[in]] said bacterium which expresses a malate dehydrogenase with decreased activity compared to the corresponding unmodified strain the *mdhA* gene has been attenuated by a modification which reduces the enzyme activity of the *mdhA* gene product.

Claim 58 (Currently Amended): The process of Claim 52, wherein said bacterium is at least one selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, [[,]] *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

Claim 59 (Currently Amended): The process of Claim 49 52, wherein said bacterium is at least one selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

Claim 60 (Currently Amended): The process of Claim 49 52, wherein said bacterium further comprises at least one gene whose expression is enhanced [[()]] compared to an unmodified starting strain[[()]] selected from the group consisting of:

- the *dapA* gene which codes for dihydridipicolinate synthase,
- the *eno* gene which codes for enolase,
- the *zwf* gene which codes for the *zwf* gene product,
- the *pyc* gene which codes for pyruvate carboxylase, and
- the *lysE* gene which codes for lysine export.

Claim 61 (Currently Amended): The process of Claim 49 52, wherein said bacterium further comprises at least one gene whose expression is attenuated (compared to an unmodified starting strain) selected from the group consisting of:

the *pck* gene which codes for phosphoenol pyruvate carboxykinase,  
the *pgi* gene which codes for glucose 6-phosphate isomerase, and  
the *poxB* gene which codes for pyruvate oxidase.

Claim 62 (Currently Amended): The process of Claim 49 52, which is a batch process.

Claim 63 (Currently Amended): The process of Claim 49 52, which is a fed batch or repeated fed batch process.

Claim 64 (Currently Amended): The process of Claim 49 52, which is a continuous process.

Claim 65 (New): The process of Claim 44, wherein said bacterium has been modified to express a decreased amount of malate dehydrogenase

Claim 66 (New): The bacterium of claim 65, wherein said malate dehydrogenase has the N-terminal amino acid residues shown in SEQ ID NO: 1.

Claim 67 (New): The bacterium of claim 66, wherein said malate dehydrogenase comprises the amino acid sequence of SEQ ID NO: 3.

Claim 68 (New): The bacterium of claim 67, wherein said malate dehydrogenase is encoded by a polynucleotide comprising the nucleotide sequence 536 to 1519 of SEQ ID NO: 2.

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Claim 69 (New): The bacterium of claim 68, wherein said polynucleotide comprises  
SEQ ID NO: 2.